

Figure 1: Full-length Sequence of *C. pneumoniae* 76kDa Gene.

ataaaaatcctt	taaaaacagg	ctcgcatata	ttattagtga	gagctttttt	ttttttttt	60
ataataaaaac	taaaagattt	ttattatttt	ttgagttttt	atg gtt aat cct att		115
				Met Val Asn Pro Ile		
				1	5	
ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt						163
Gly Pro Gly Pro	Ile Asp Glu Thr Glu Arg Thr	Pro Pro Ala Asp Leu				
	10	15	20			
tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct						211
Ser Ala Gln Gly Leu Glu Ala Ser	Ala Ala Asn Lys Ser	Ala Glu Ala				
	25	30	35			
caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat						259
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp						
	40	45	50			
tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg						307
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met						
	55	60	65			
agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct						355
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser						
	70	75	80	85		
act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg						403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr						
	90	95	100			
cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct						451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala						
	105	110	115			
tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct						499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala						
	120	125	130			
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct						547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala						
	135	140	145			
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc						595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala						
	150	155	160	165		
gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct						643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala						
	170	175	180			
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc						691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe						
	185	190	195			

Figure 1 (continued)

gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200 205 210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro-Asp Ser Pro Ile Leu	
295 300 305	
caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Val	
330 335 340	
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc	1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser	
345 350 355	
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct	1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser	
360 365 370	
ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct	1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser	
375 380 385	
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc	1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala	
390 395 400 405	
gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct	1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala	
410 415 420	

Figure 1 (continued)

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn	
425 430 435	
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct	1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro	
440 445 450	
ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag	1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys	
455 460 465	
acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt	1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly	
470 475 480 485	
tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat	1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn	
490 495 500	
gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca	1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr	
505 510 515	
cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca	1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr	
520 525 530	
gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga	1747
Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly	
535 540 545	
gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc	1795
Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile	
550 555 560 565	
cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca	1843
Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr	
570 575 580	
tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt	1891
Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu	
585 590 595	
tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt	1939
Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe	
600 605 610	
gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa	1987
Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu	
615 620 625	
acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta	2035
Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu	
630 635 640 645	

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Figure 1 (continued)

tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 2083
Tyr Ser Gly Tyr Leu Gln
650

ttattatgtg ctttggttaag gcctttgttg aggccttacc aacacactag aacgatcttc 2143

aataaataaaa aga 2156

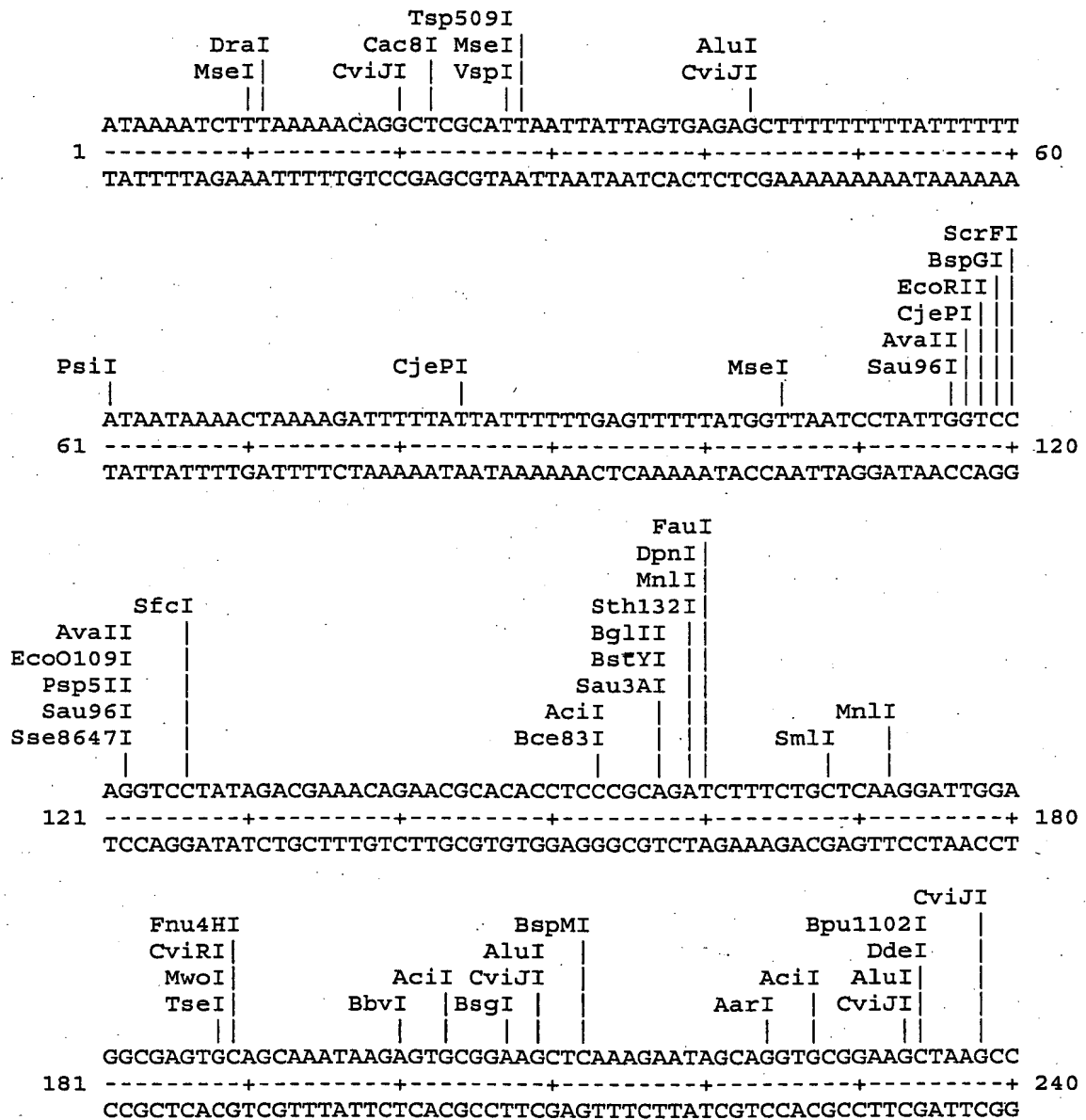
Figure 2: Restriction enzyme map of *C. pneumoniae* 76kDa gene.

Figure 2 (continued)

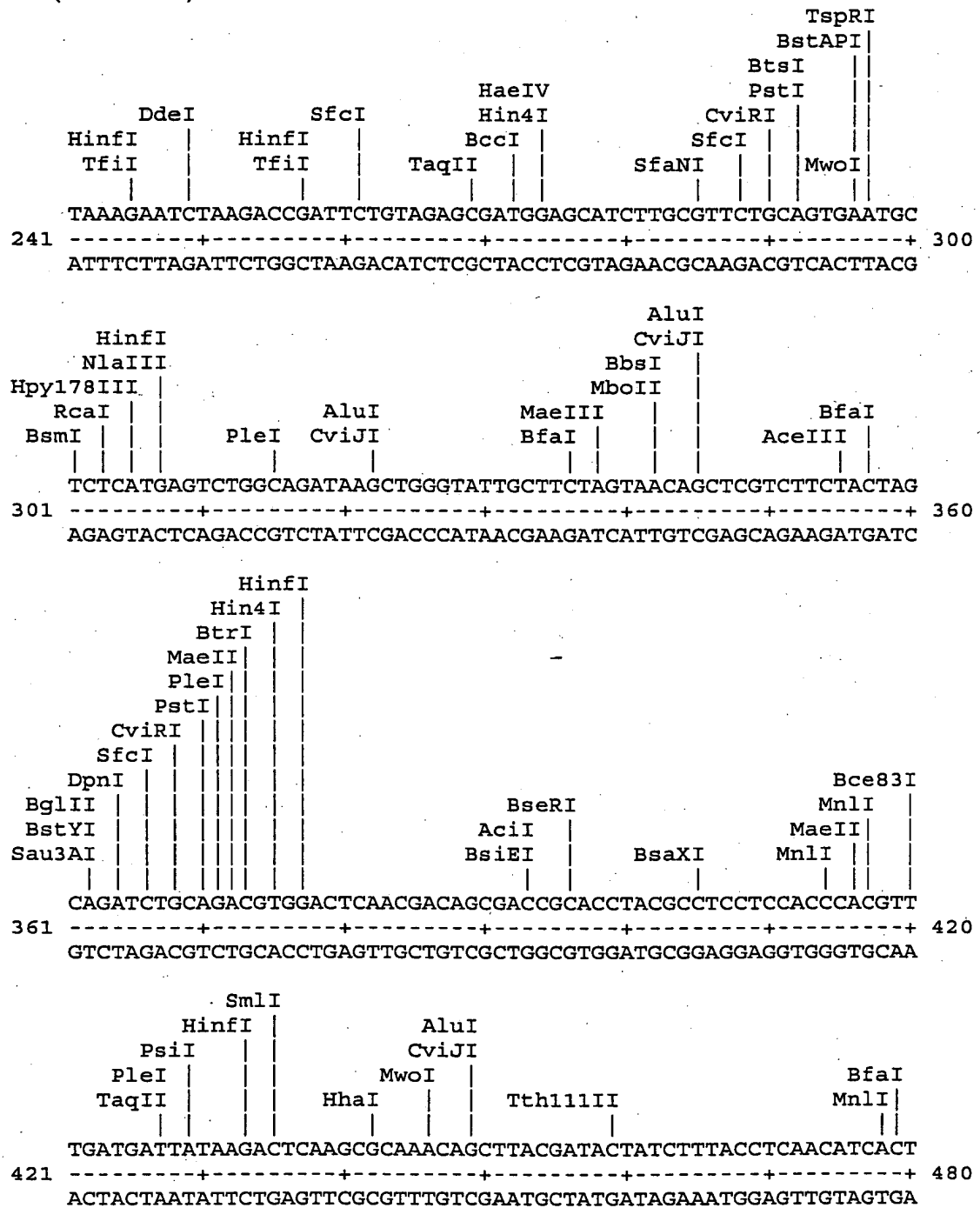


Figure 2 (continued)

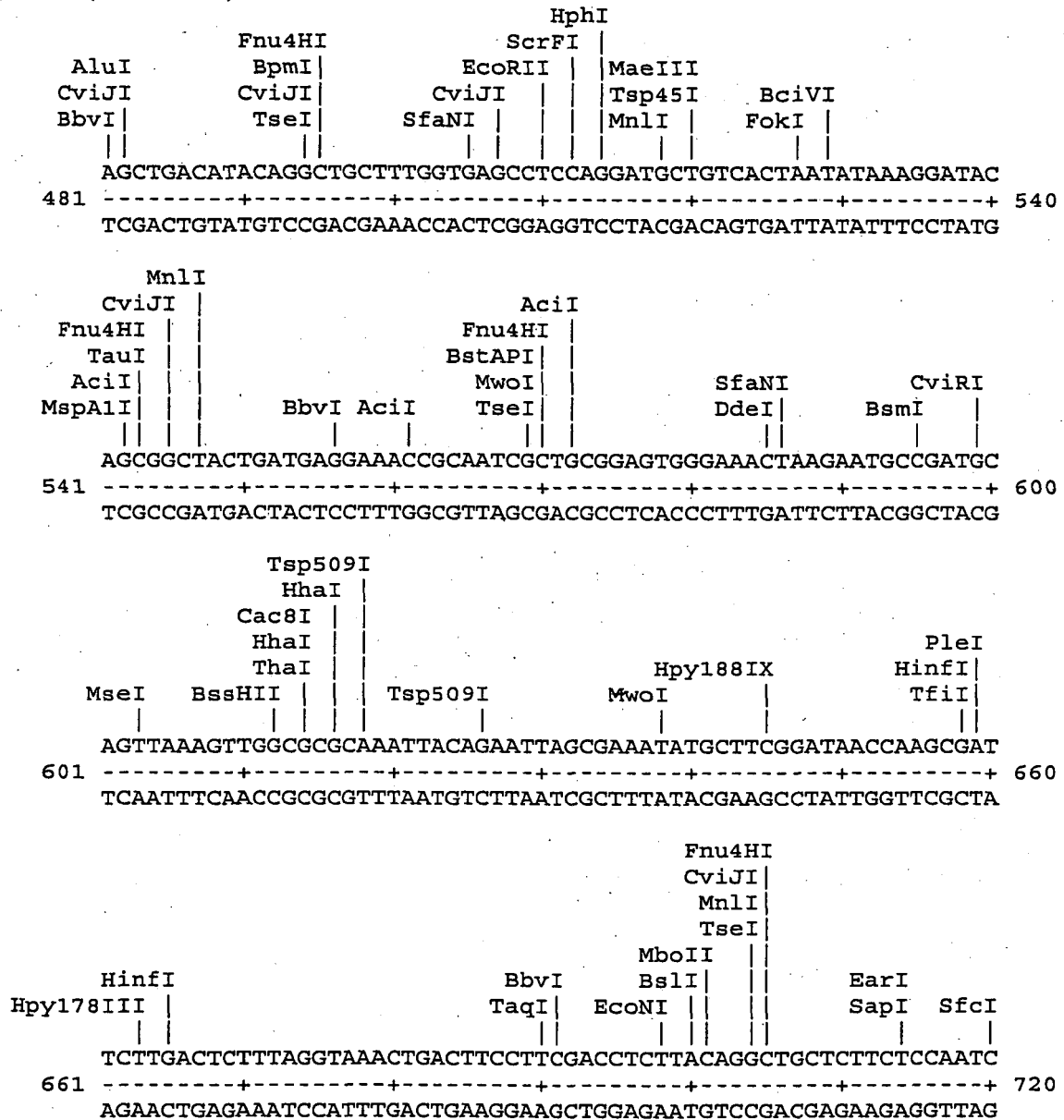


Figure 2 (continued)

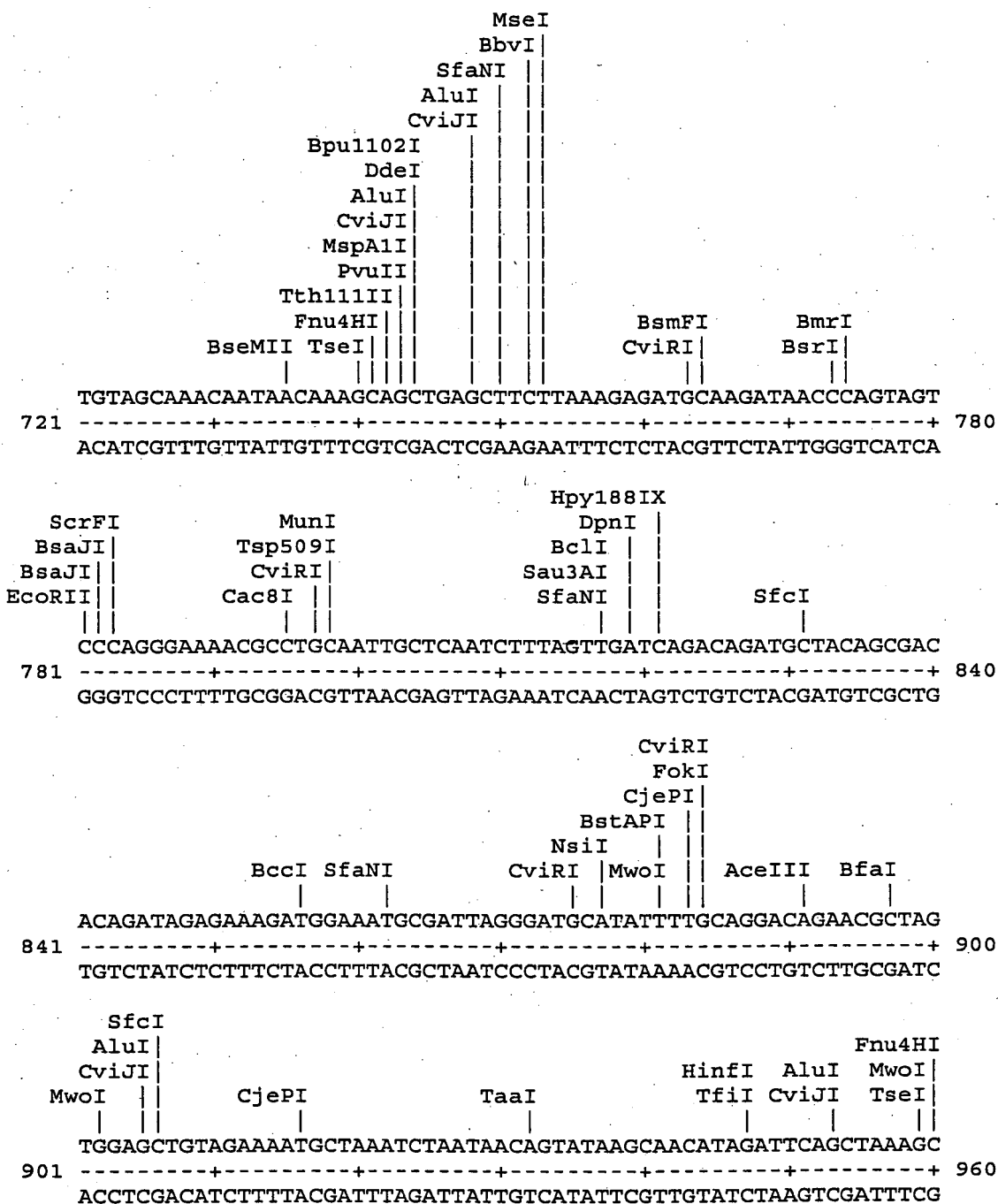
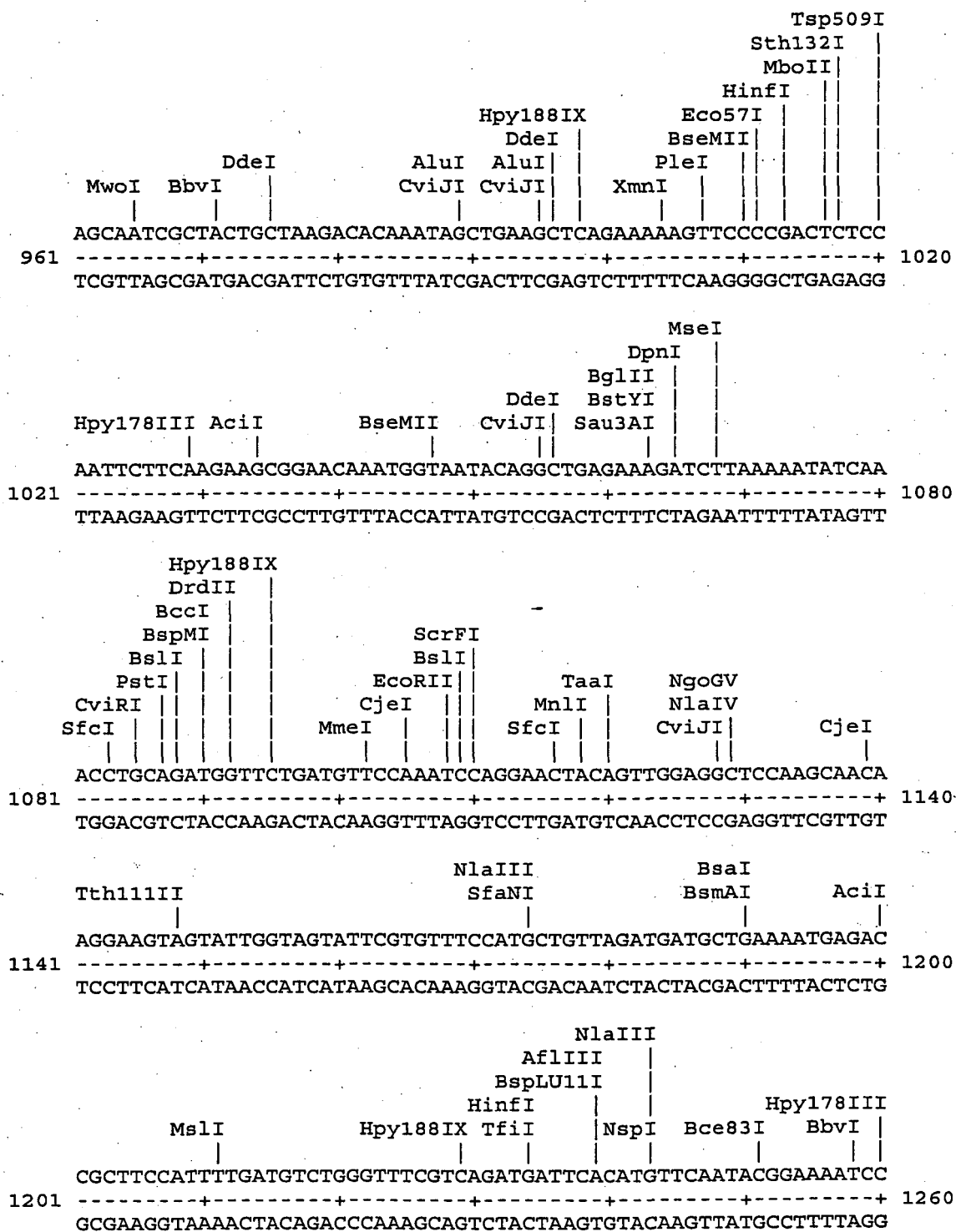


Figure 2 (continued)



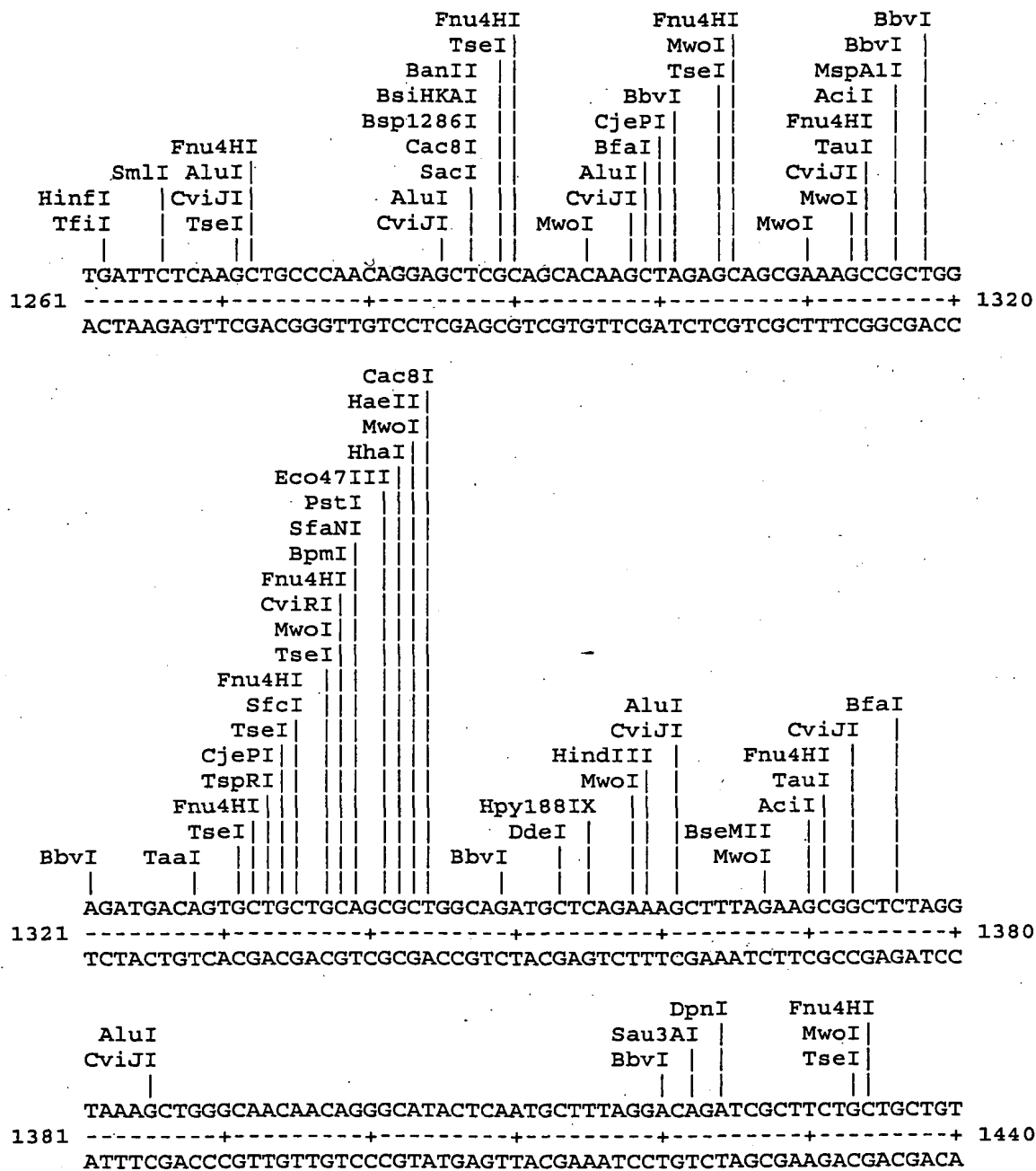


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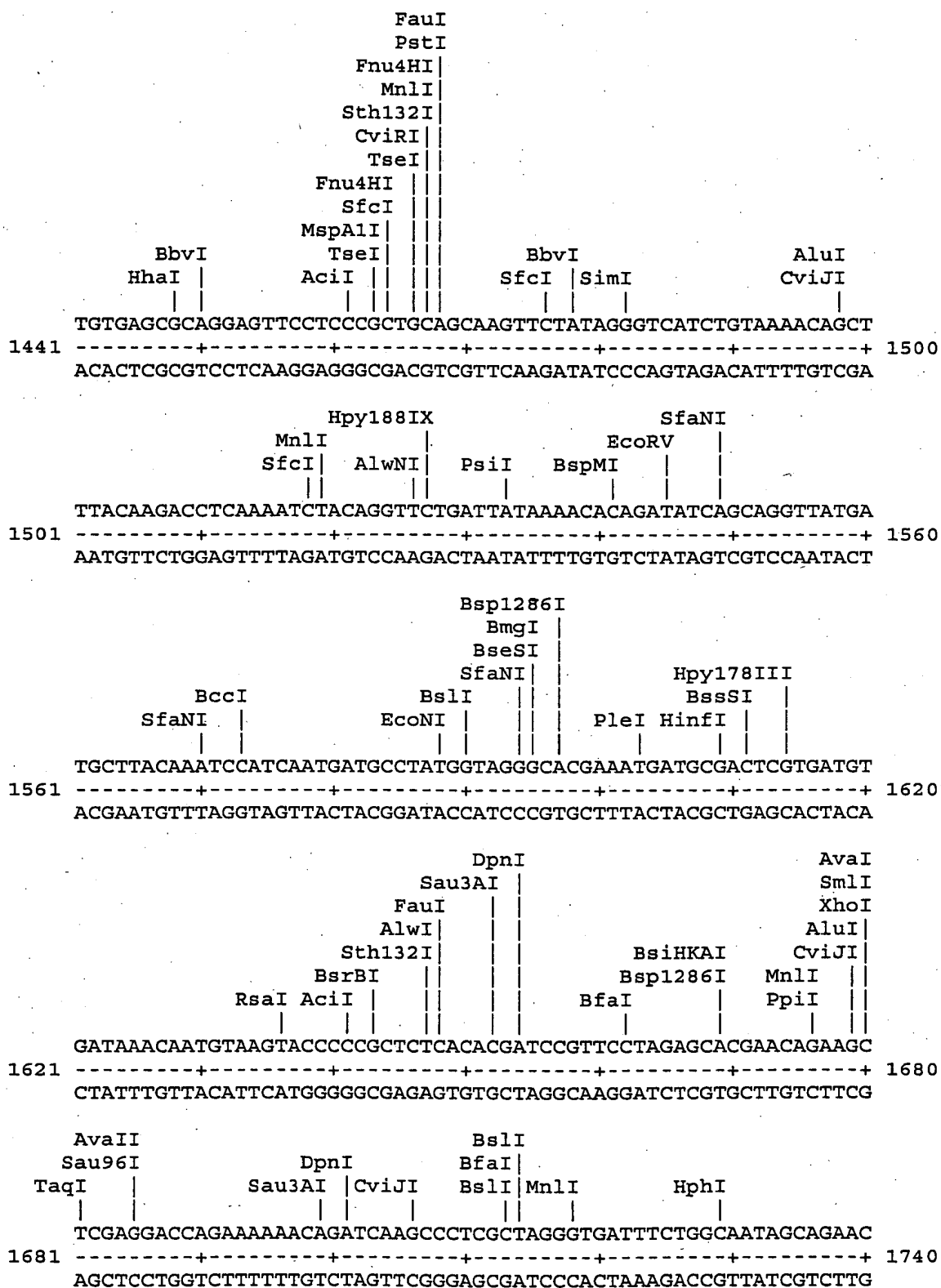


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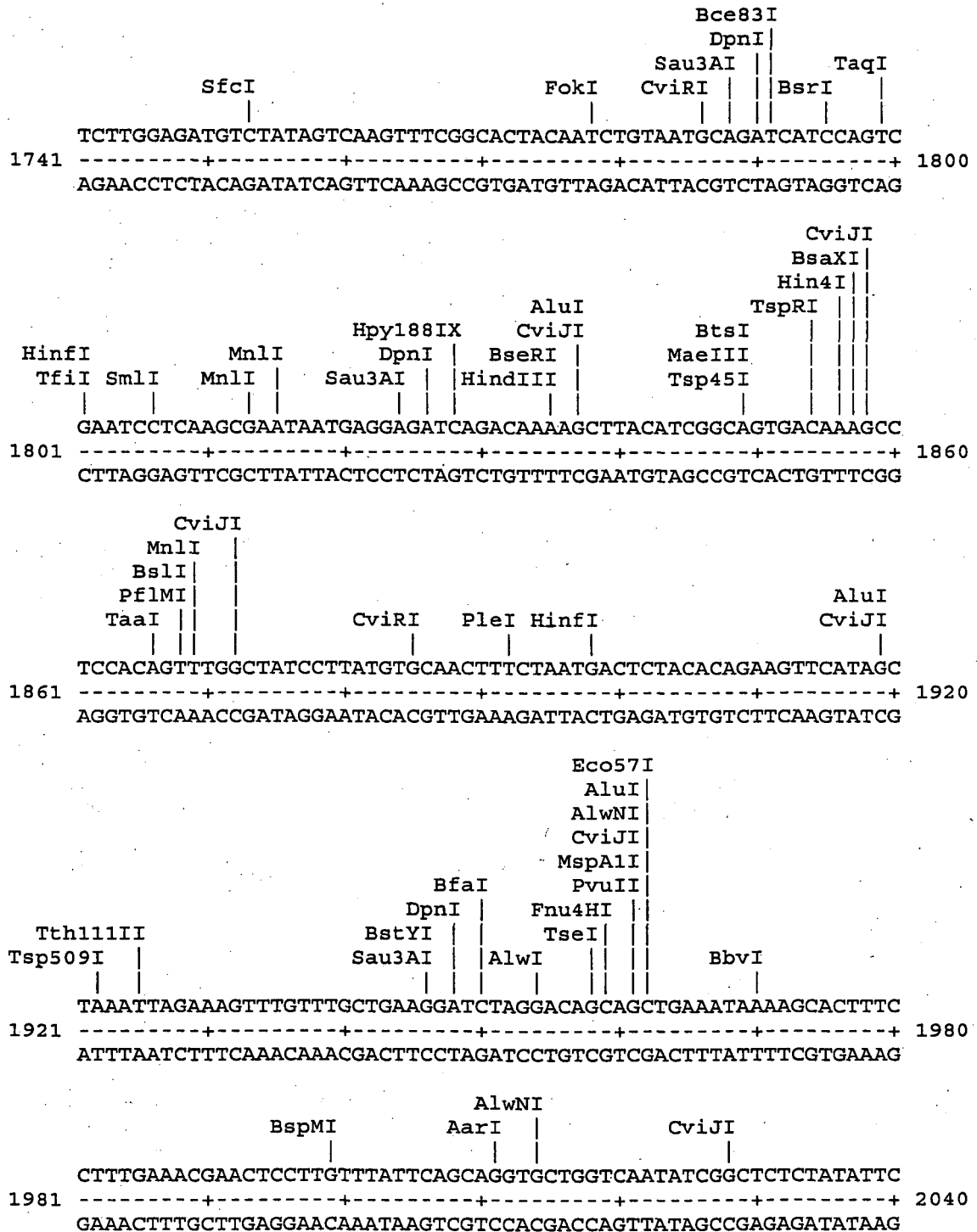


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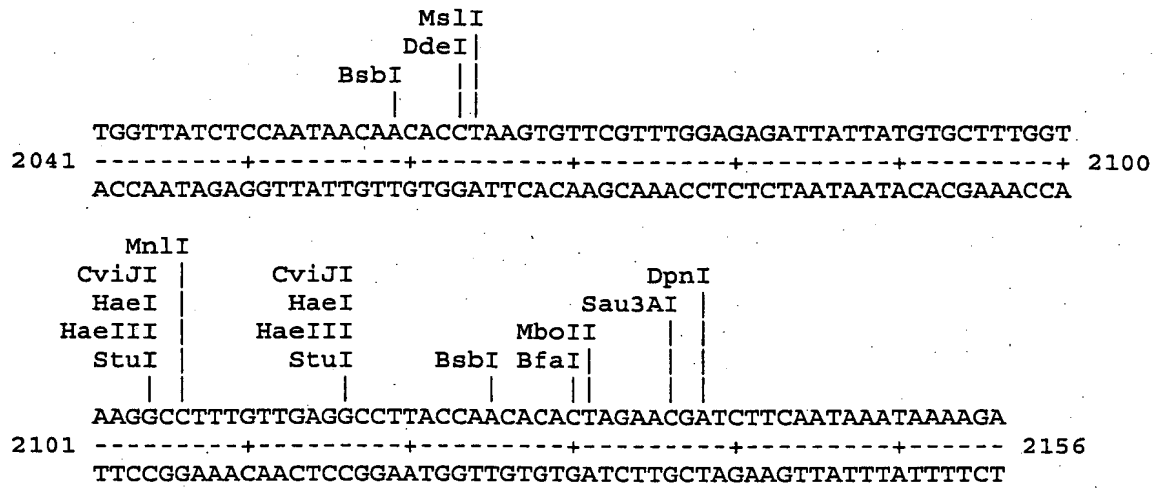


Figure 3: Sequence Containing Truncated Version of *C. pneumoniae* 76kDa Gene; (nucleotides 1 to 665 and 2122 to 2238 are unrelated to the 76kDa Gene).

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atgacaaaaa aacattatgc ttgggttgta gaagggatc tcaatcgttt gcctaaacag 60
ttttttgtga aatgtagtgt tgtcgactgg aacacattcg ttccttcaga aacctccact 120
acagaaaaag ctgctacaaa cgctatgaaa tacaaatact gtgtttggca gtggctcgtc 180
ggaaagcata gtcagggttcc ttggatcaat ggacagaaaa agcctctata tctttatgga 240
gctttcttaa tgaacccttt agcaaaggct acgaagacta cgtaaagtgg aaaagaaaac 300
ctagcttggt ttattggagg aactttaggg ggactcagaa aagctggaga ctggctcgcc 360
acagtacggt atgagtatgt cgaagccttg tcggttccag aaatagatgt ttcagggatt 420
ggccgtggta atttattaaa gttttggttc gcccaagcaa ttgctgctaa ctatgatcct 480
aaagaggcta atggttttac aaattataaa ggattttccg ctctatatat gtatggcatc 540
acagattctc tatcattcag agcttatggg gcttactcca aaccagcaaa cgataaactc 600
ggcagtgatt ttactttccg aaagtttgat ctagggtataa tttcagcggt ttaagtcaaa 660
ttttaataaa atctttaaaa acaggctcgc attaattatt agtgagagct ttttttttat 720
tttttataat aaaactaaaa gattttttatt atttttttgag ttttt atg gtt aat cct 777
                                         Met Val Asn Pro
                                         1

att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat 825
Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp
   5              10              15              20

ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa 873
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu
              25              30              35

gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc 921
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr
              40              45              50

gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc 969
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu
              55              60              65

atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct 1017
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser
              70              75              80

tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct 1065
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro
   85              90              95              100

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Figure 3 (continued)

acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca	1113
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr	
105 110 115	
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct	1161
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala	
120 125 130	
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg	1209
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala	
135 140 145	
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat	1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn	
150 155 160	
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat	1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr	
165 170 175 180	
gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc	1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser	
185 190 195	
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac	1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn	
200 205 210	
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca	1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro	
215 220 225	
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct	1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala	
230 235 240	
aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	1545
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
245 250 255 260	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	1593
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
265 270 275	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	1641
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
280 285 290	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	1689
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
295 300 305	

Figure 3 (continued)

[illegible]

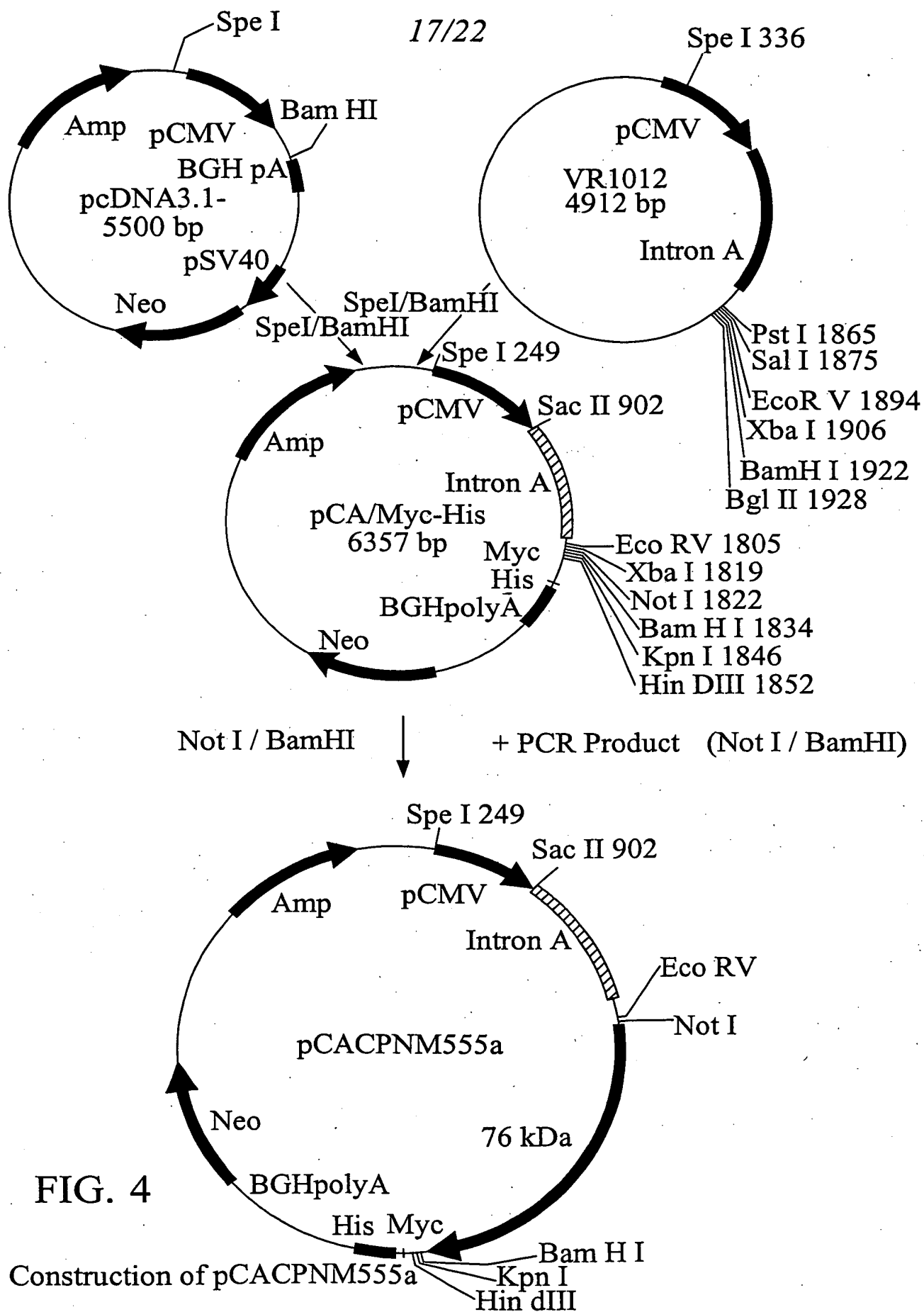


FIG. 4

Construction of pCACPNM555a

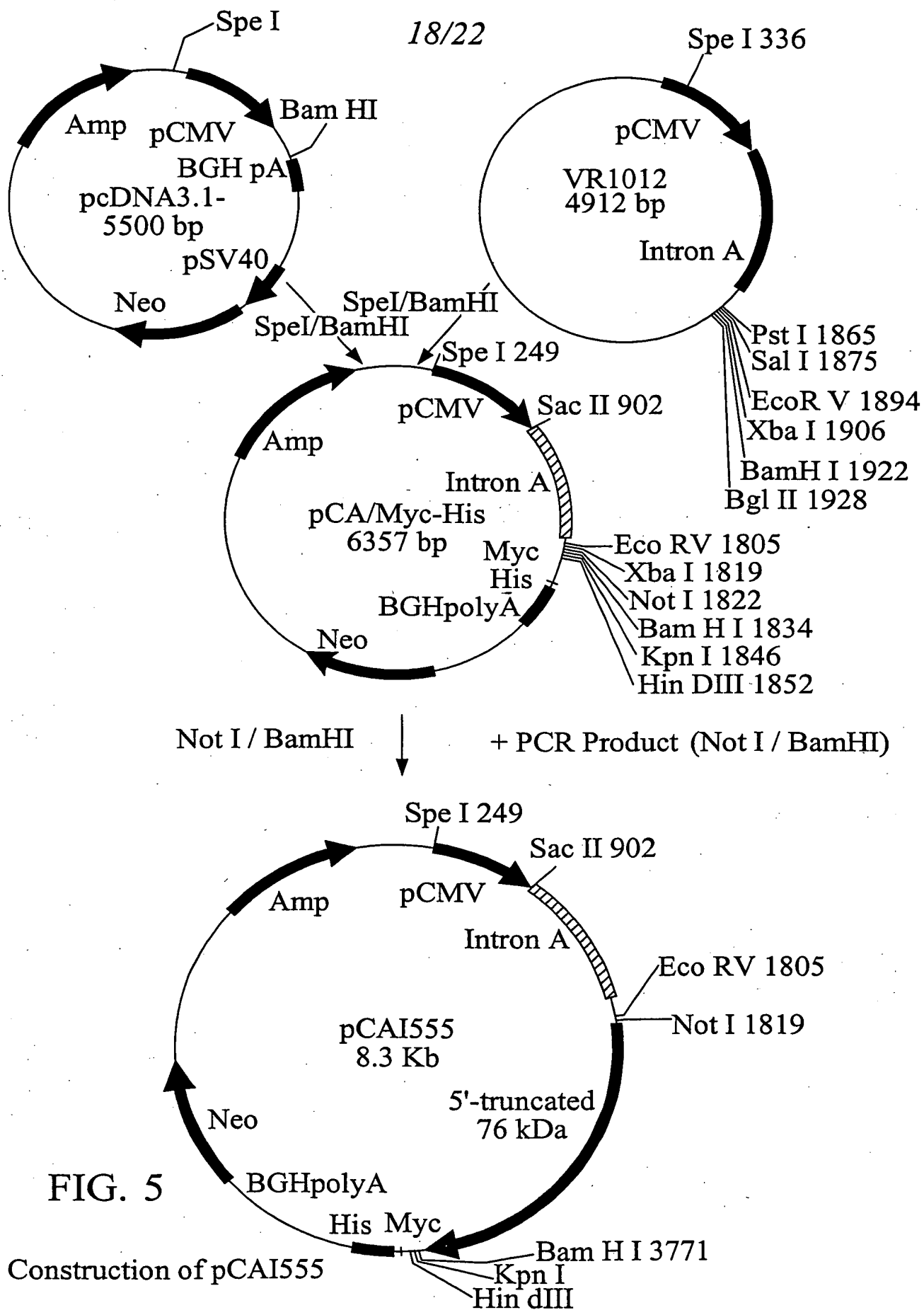


FIG. 5
Construction of pCAI555

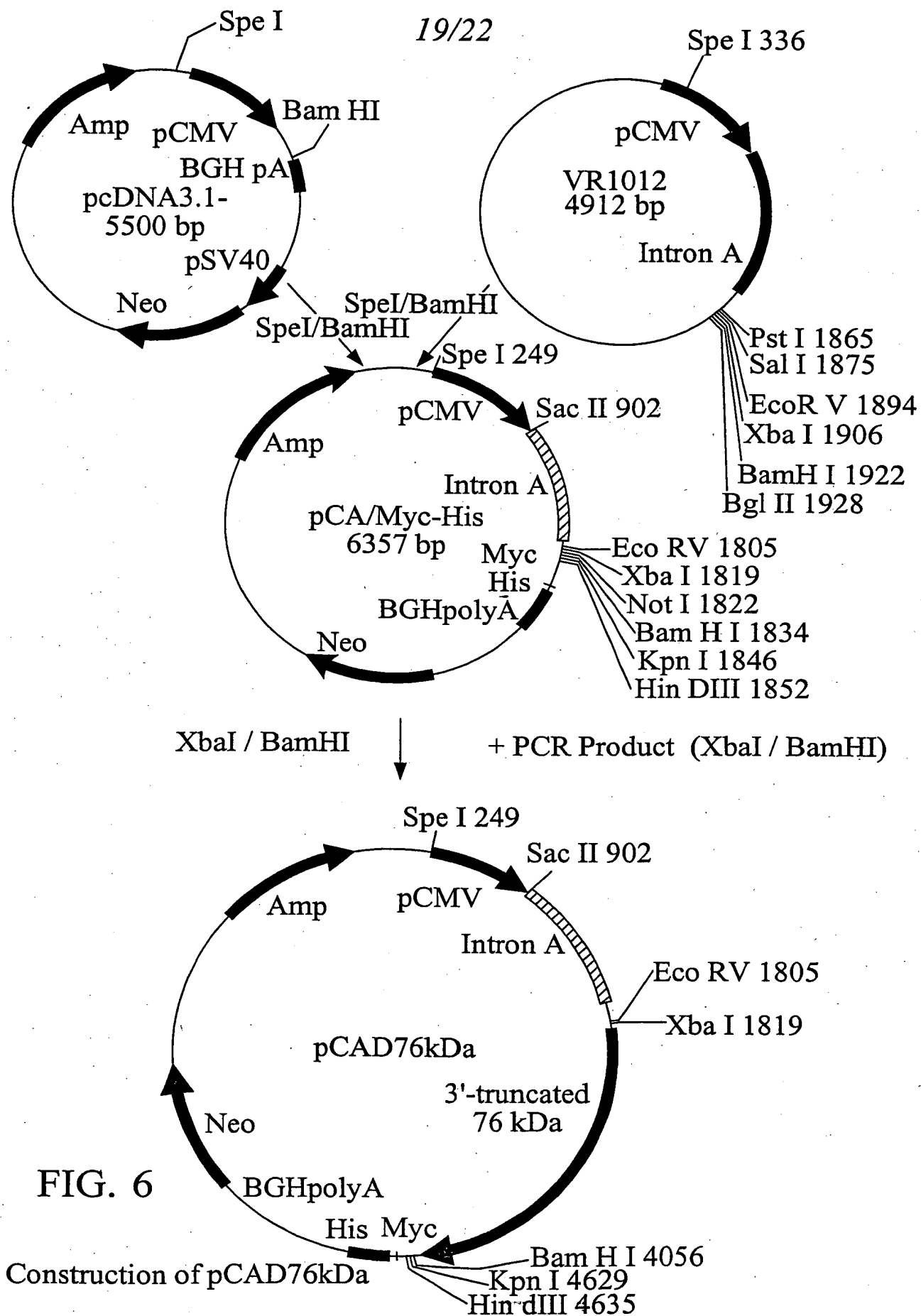


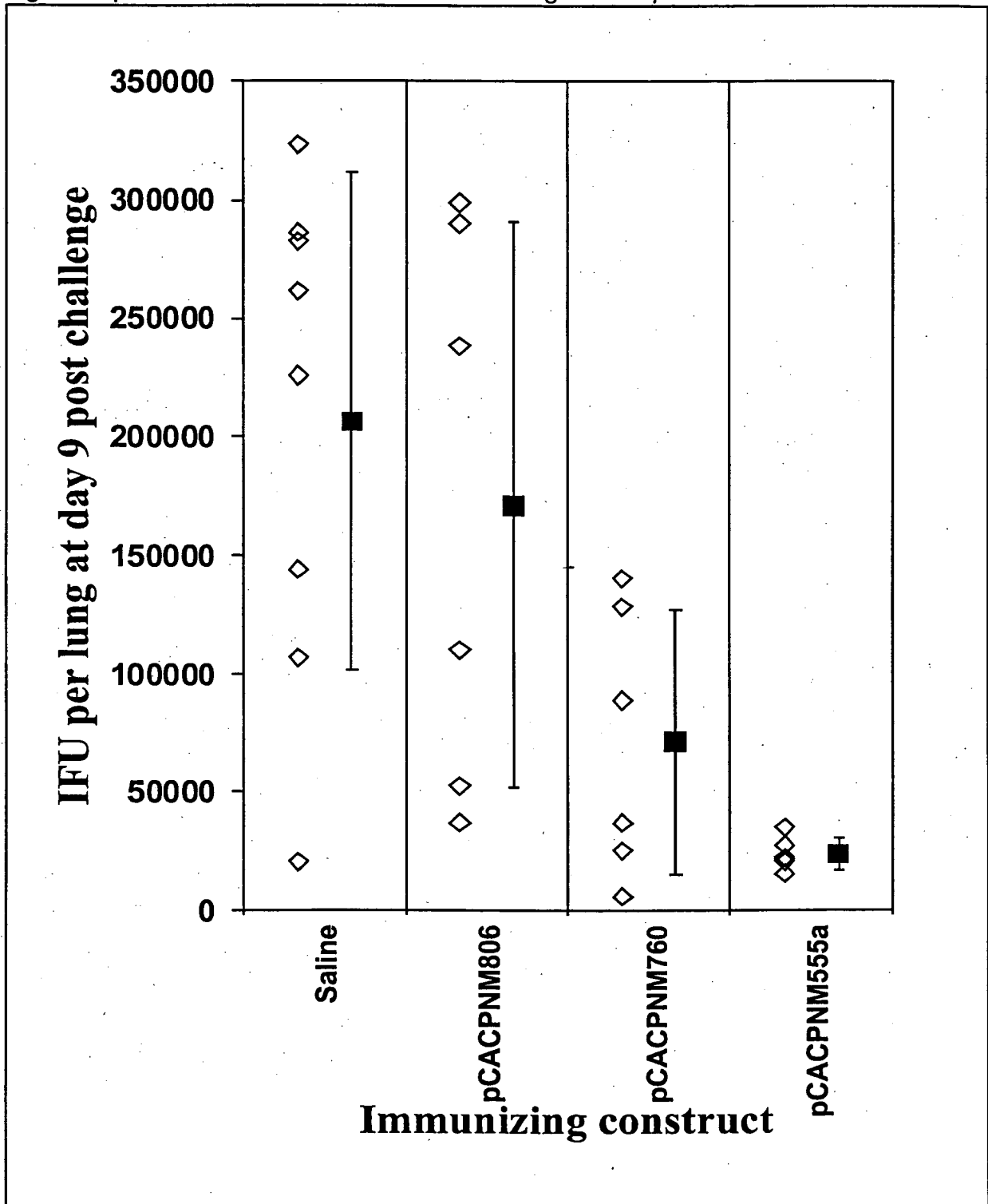
Figure 7: pCACP NM555a Confers Protection Against *C. pneumoniae* Infection .

Figure 8: pCAI555 Confers Protection Against *C. pneumoniae* Infection.

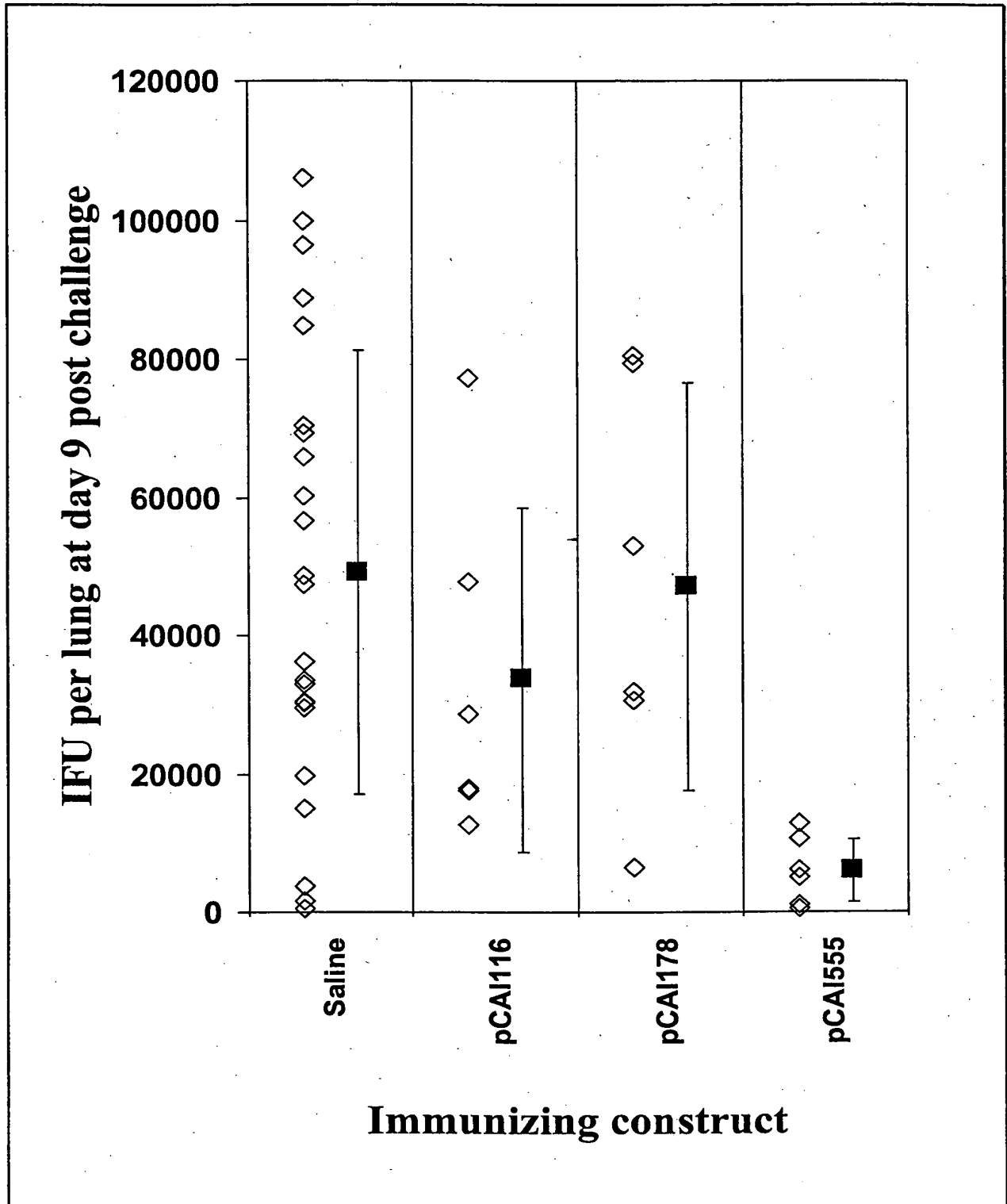


Figure 9: pCAD76kDa Confers Protection against *C. pneumoniae* Infection.

